

$\frac{1}{11}$

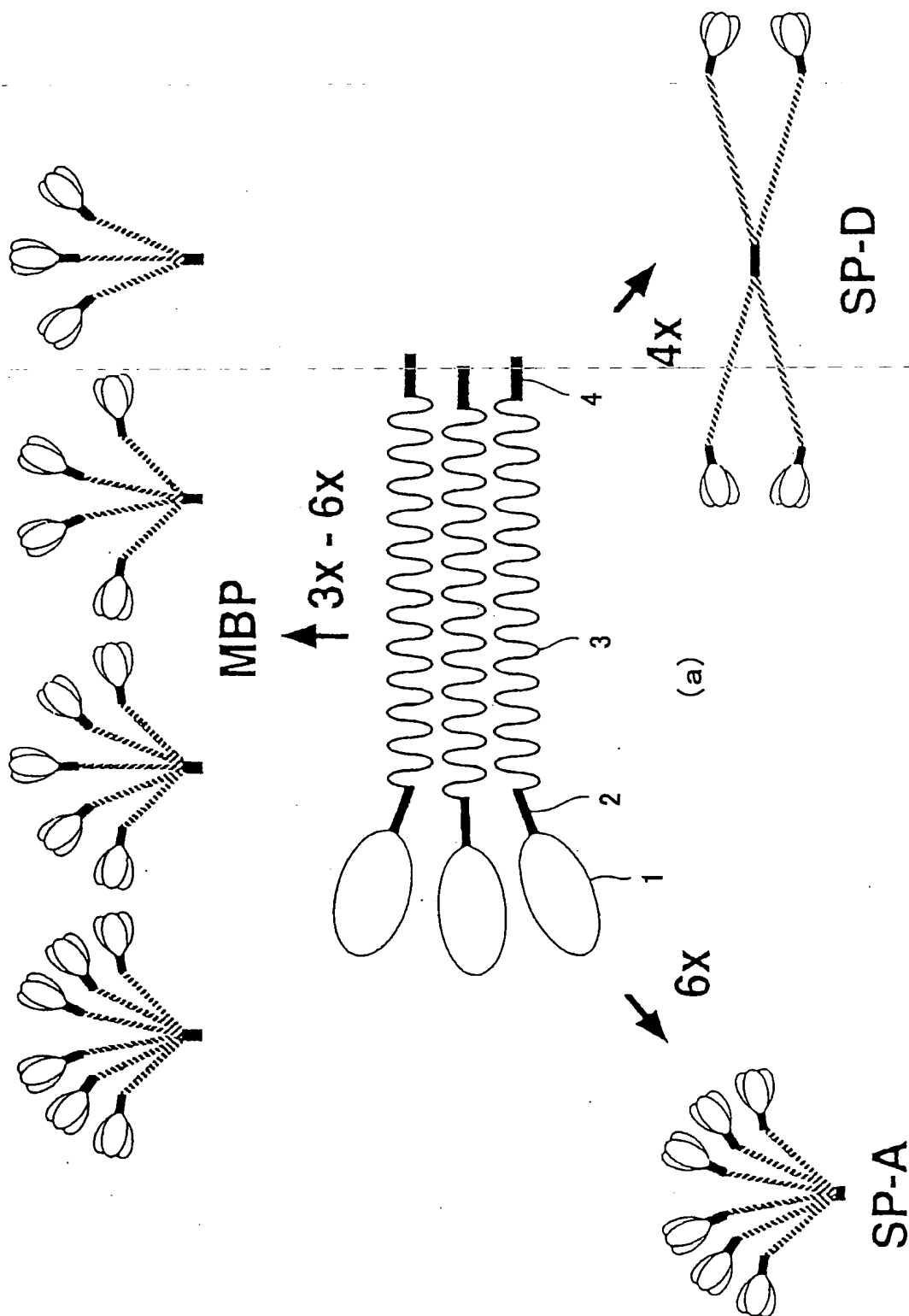
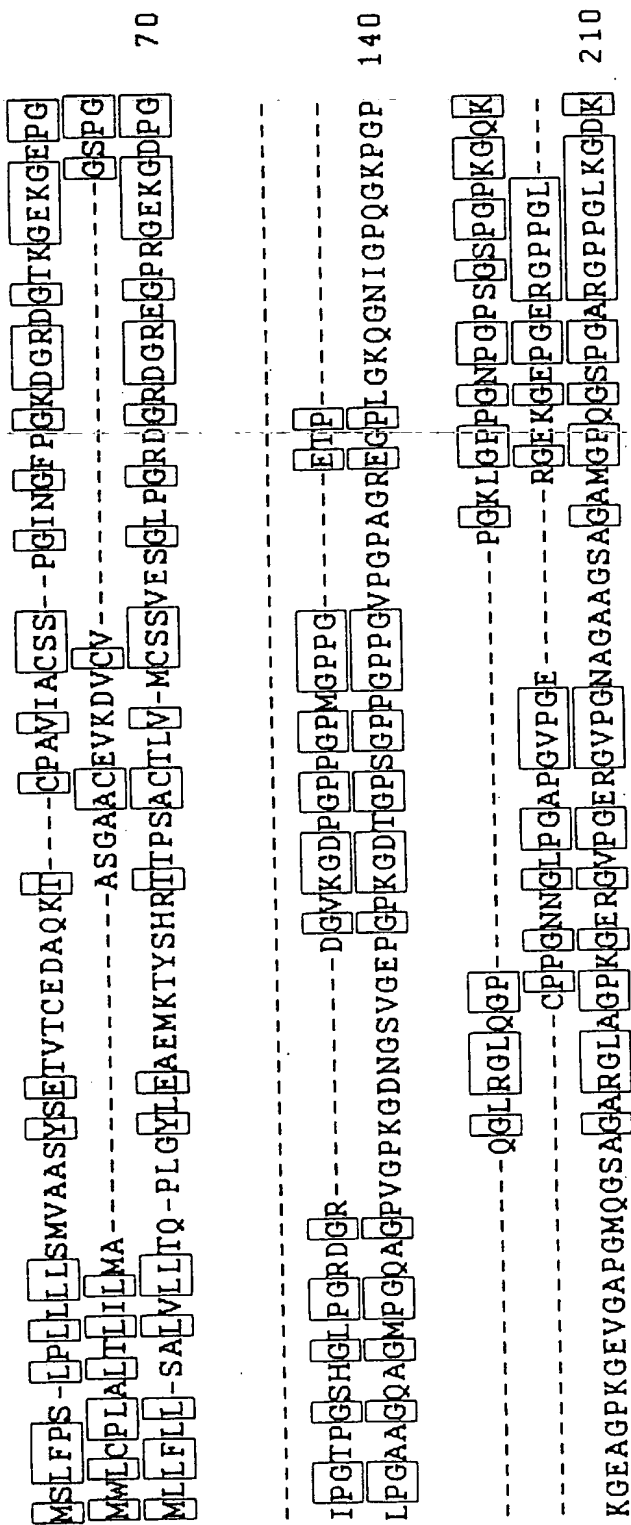


Fig. 1

human MBP  
human SP-A  
human SP-D



2/11

Fig. 2

human MBP  
human SP-A  
human SP-D

GDPG-KSPDGDSSLA--SERKALQTEMARIKKWLTFSLGKQVGNKFFLTNGEIMTFEKV  
--PAHLDEELQATLHD--FRHQILQTRGALS-LQGS-----MTVGEKVFSSNGQSIITFDAL  
GIPGDKGAKGESGLPDVASLRQQVEALQGGVQHLQAQAFSQYKKVLEFPNGQSVGEKIFKTAGFVKPFTEA 280  
KALCVKFQASVAIPRNAENGAIQNLII--KEEAFGLITDEKTEGQFVDLTGNRLITYTNWNEGEPNNAGS  
QEACARAGGRIAVPRNPEENEAIASFVKKKYNTYAYVGLTEGSPGDFRYSDGTPVNTYNWYRGEPARG-  
QLLCTQAGQLASPRSAENALQLLVAKNEAFLSMTDSKTEGKFTYPTGESLVYSNWAPEGPNDDGG 350  
DEDCVLLKNGQWNDVPCSTSHLAVCEFP I\*  
KEQCVEMYTDGQWNDNRNCLYSRLTICEF\*--  
SEDCVEIFNGKWNDRACGEKRLVVCFF\*--

3/11

09/763712

Fig. 3



5/11

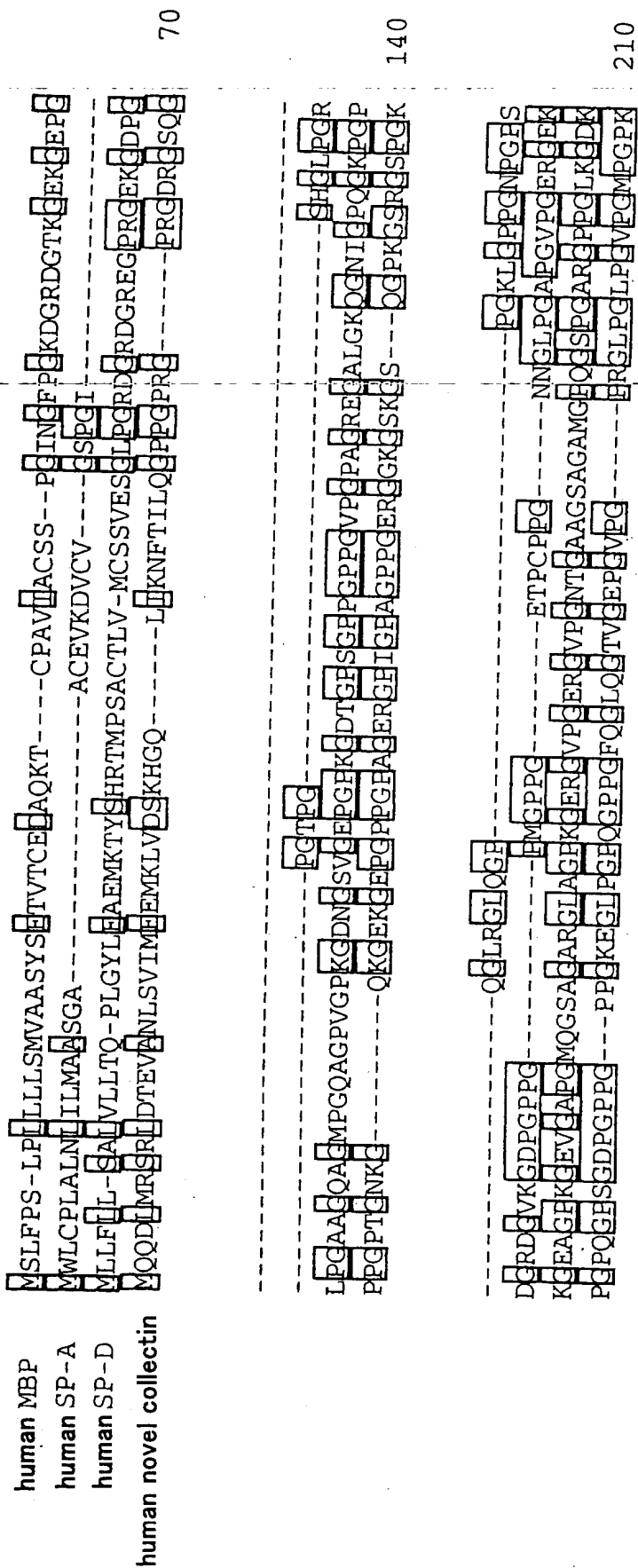


Fig. 5

human MBP  
human SP-A  
human SP-D  
human novel collectin

CSPGHKQKQKGDPCSPDG---DSSLAAASERKALQTEMARIKKWLTFSLG--KQVGNKFFFLTNGEIMTTEK  
 CEAGERGH---PGLPA---HLDEELQATLHDFRHQILQTRGALSLOGSIMTVGEKVFSSNGQSITIDA  
 QIPGDKAKGESGLPDVASLRQQVEALQGVQHLQAAFQYKKVELFNG--QSVGEKIFKTAGFVKPTE  
 QPPGHPCG---SCAVVPLALQNEPTPAEDNGC-----PQHWKNFTDKCYVFSVKEIFEED  
 280

VKALQVKFQASVATPRNAANGALQNLII---KEEAFLEITTEKTEGQFVDLIGNRLTYTNMNEGEENN--  
 IQEACARAGGRIAVPRNPEENEALASFKKYNITYAYVGLTEGSPGDFRYS DGTPEVNYTNWYRCGEAG--  
 AQLLQTOAGGQLASPRSAANEALQQLVMKAKNEAAFLSMTDSKTEGKFTYPTGESLVMSNMAPCEEND--  
 AKLFCEDKSSHVLFINTREEQQWIKKQMMG--RESHWIGLTDSEENNEWKWL DGTSPDYKNWKAGQDFDNG  
 350

--ACSDQEDCVLLKNGOWNLVPCSTSHLAVCEFFPI\*-----  
 --RC-KEEQVEMYTDGOWNDRNQLYSRLTICDF\*-----  
 --DGGSEDCVEIFTNCKWNDRACGEKRLVVCFF\*-----  
 HGHCPGEDCAGLIYAGOWNLFQCEDVNNFLCEKDRFVLSAL\*

Fig. 6

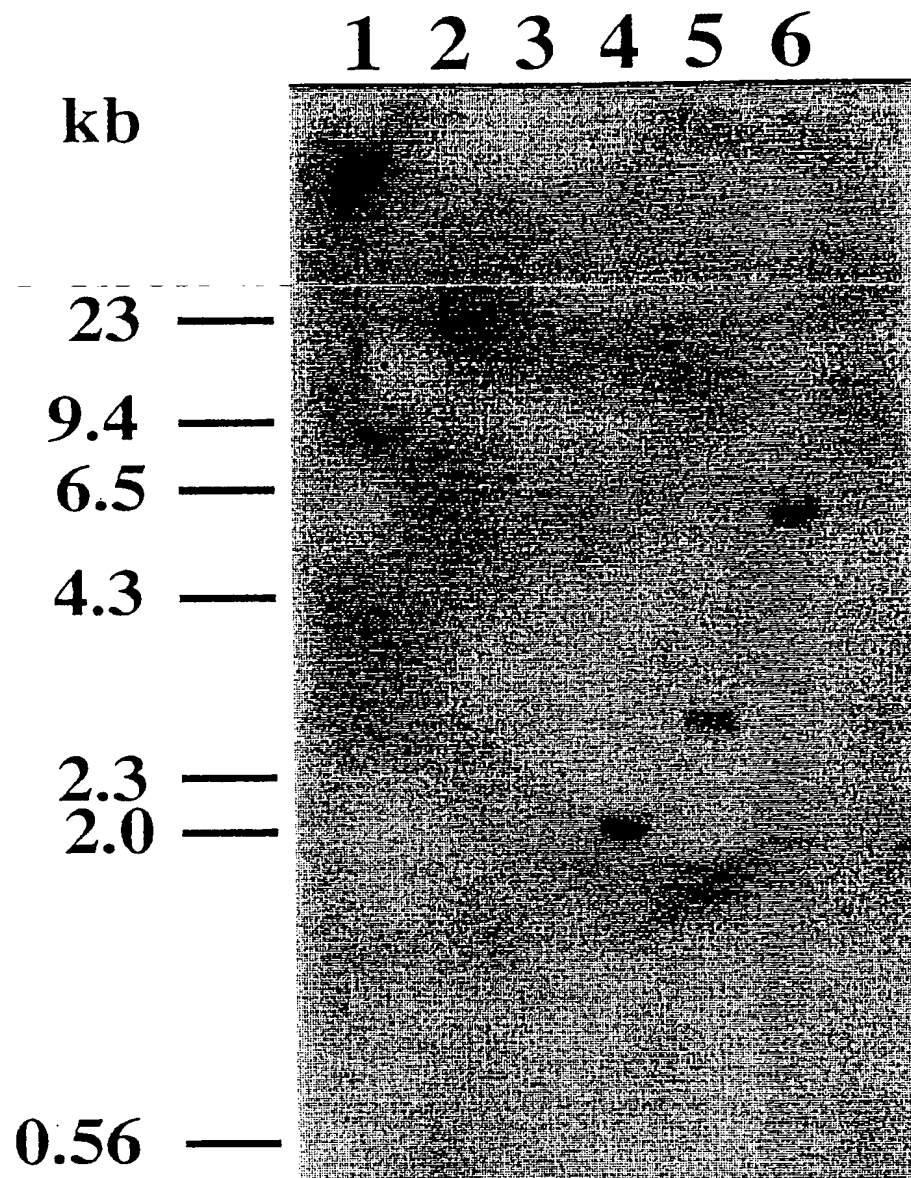
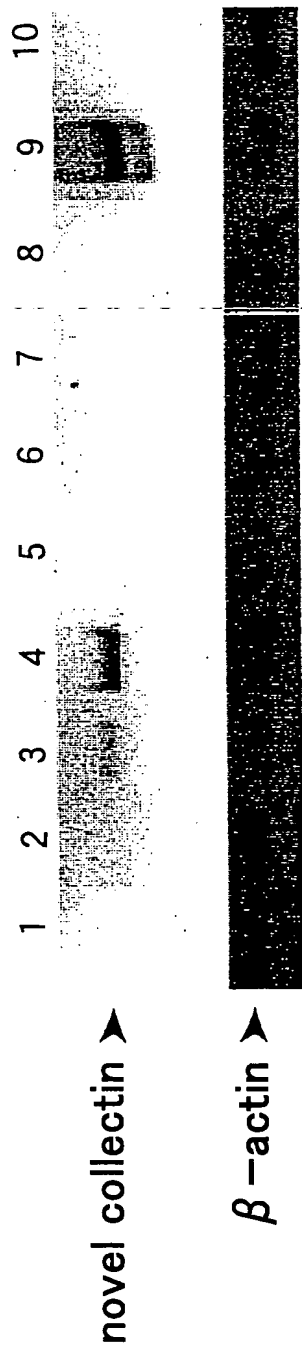
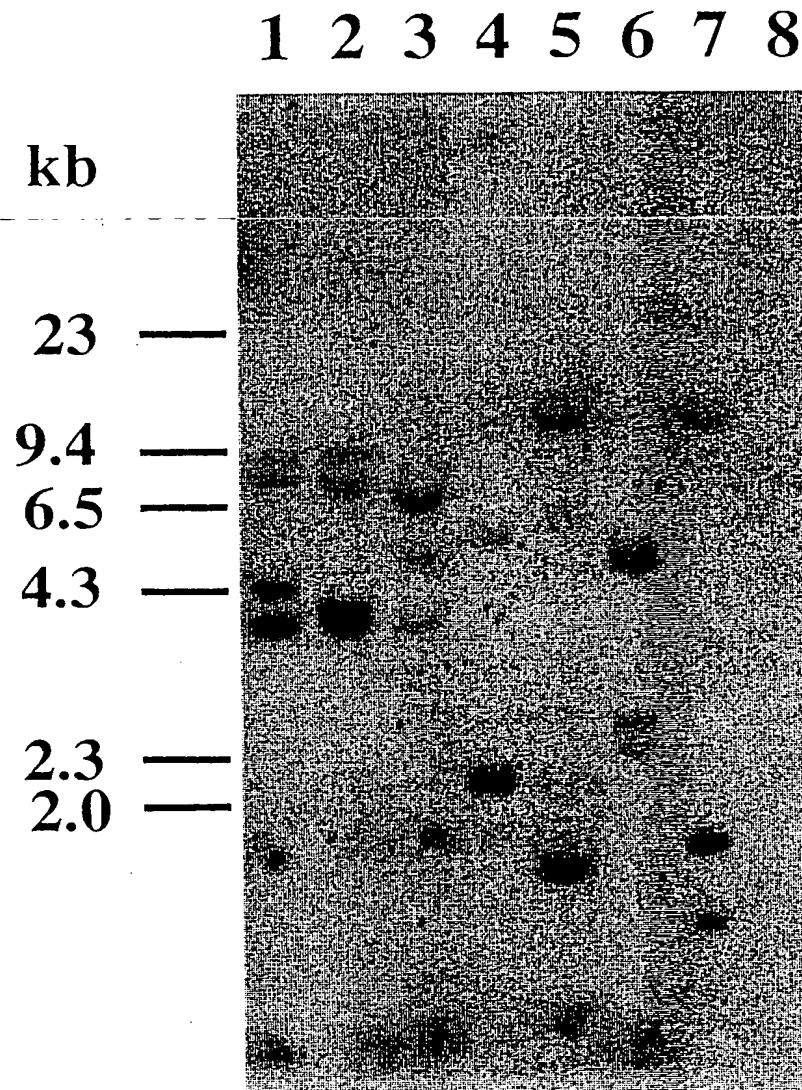
$\frac{7}{11}$ 

Fig. 7



٨٠٠



$\frac{9}{11}$ **Fig. 9**

10/11

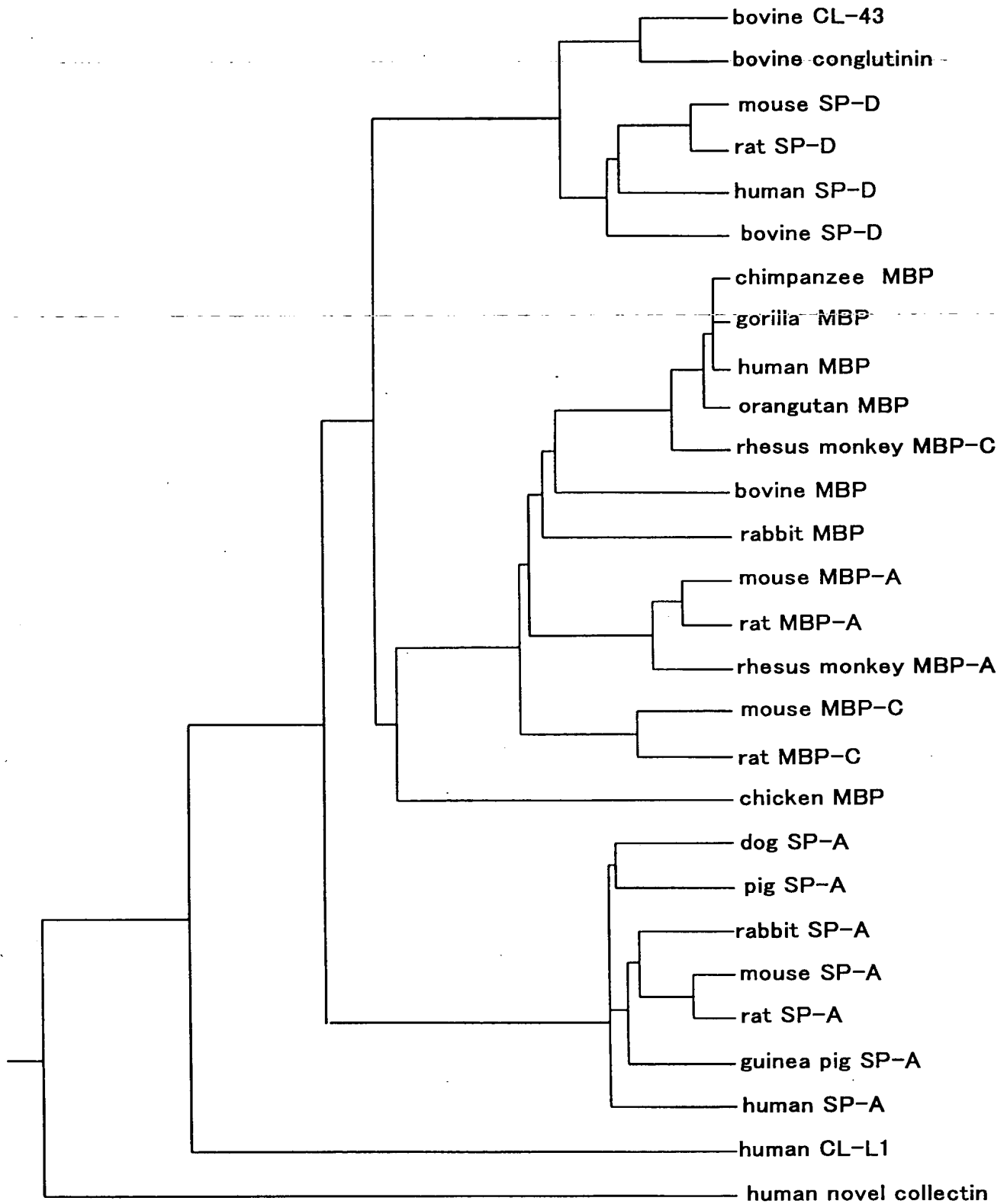


Fig. 10

11/11

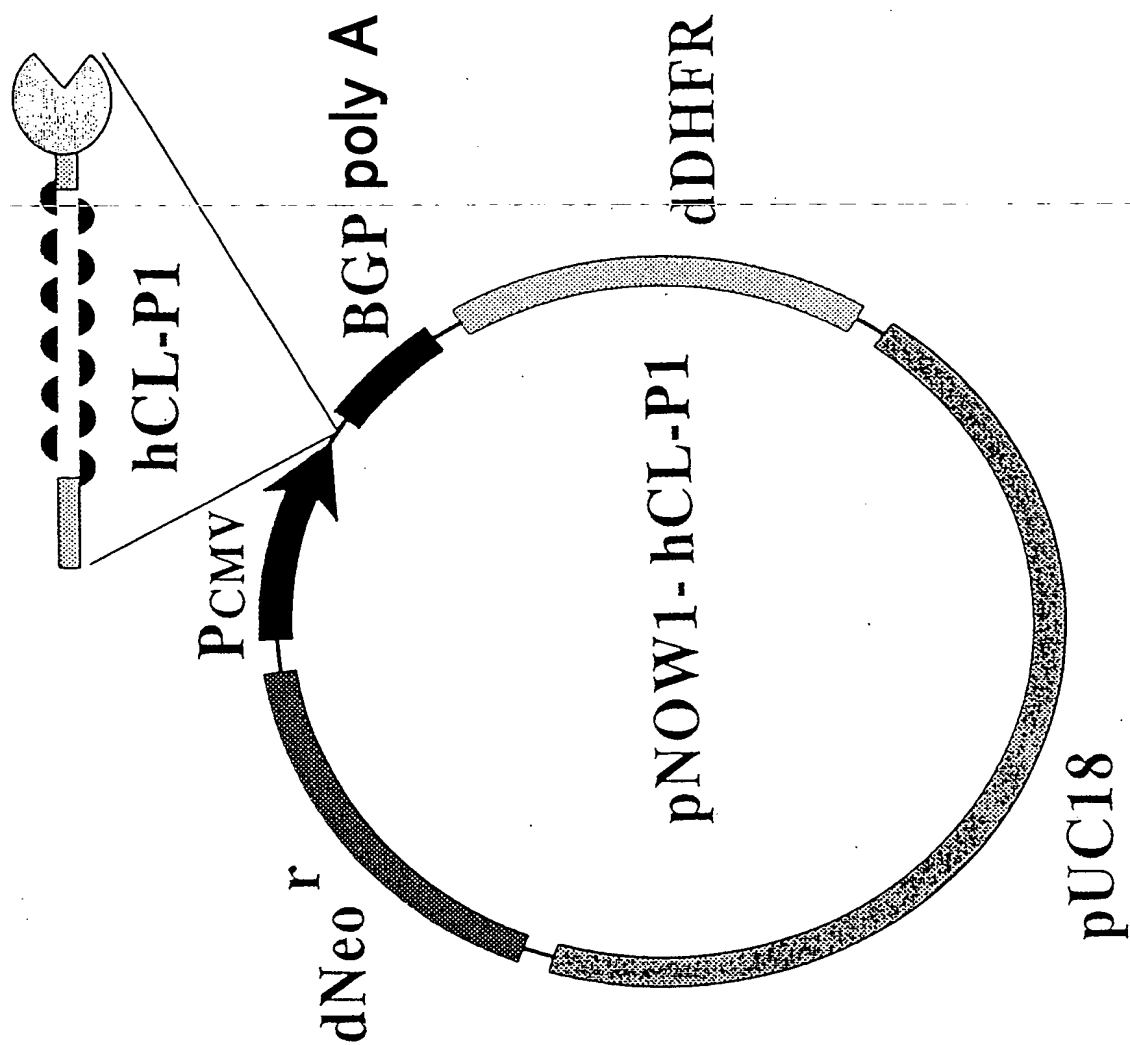


Fig. 11